

SEQUENCE LISTING

<110> Vadim R. Viviani
Yoshihiro Ohmiya

<120> Nucleic Acid Molecules Encoding Red and
Green Emitting Luciferases

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<140> 09/516,958

<141> 2000-03-01

<150> 09/388,290

<151> 1999-09-01

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Glu Arg Pro Arg Asp Ile Val His Pro Gly Ser Ala Gly Gln Gln Leu	
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Tyr Gln Ser Leu Tyr Lys Phe Ala Ser Phe Pro Glu Ala Ile Ile Asp	
30 35 40	
gct cat aca aat gaa gta ata tca tat gct caa ata ttt gaa acc agc	196
Ala His Thr Asn Glu Val Ile Ser Tyr Ala Gln Ile Phe Glu Thr Ser	
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Cys Arg Leu Ala Val Ser Ile Glu Gln Tyr Gly Leu Asn Glu Asn Asn	
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gtt gtg ggt gta tgc agt gaa aac aat ata aac ttt ttt aat cct gtc	292
Val Val Gly Val Cys Ser Glu Asn Asn Ile Asn Phe Phe Asn Pro Val	
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Leu Ala Ala Leu Tyr Leu Gly Ile Pro Val Ala Thr Ser Asn Asp Met	
90 95 100 105	
tac aca gat gga gag tta act ggt cat ttg aat ata tca aaa cca act	388
Tyr Thr Asp Gly Glu Leu Thr Gly His Leu Asn Ile Ser Lys Pro Thr	
110 115 120	
atc atg ttt agt tca aag aaa gca ctc ccg ctt att ctg aga gta cag	436
Ile Met Phe Ser Ser Lys Lys Ala Leu Pro Leu Ile Leu Arg Val Gln	
125 130 135	
caa aat cta agt ttc att aaa aaa gtc gta gtt atc gat agc atg tac	484
Gln Asn Leu Ser Phe Ile Lys Lys Val Val Val Ile Asp Ser Met Tyr	
140 145 150	
gac att aat ggc gtt gaa tgc gta tct acc ttt gtt gca cgt tat act	532
Asp Ile Asn Gly Val Glu Cys Val Ser Thr Phe Val Ala Arg Tyr Thr	
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gac cac acc ttt gat cca ttg tca ttt aca cca aaa gat ttt gat ccc	580
Asp His Thr Phe Asp Pro Leu Ser Phe Thr Pro Lys Asp Phe Asp Pro	
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Leu Glu Lys Ile Ala Leu Ile Met Ser Ser Ser Gly Thr Thr Gly Leu	
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Val Asp Gln Tyr Asp Leu Ser Ser Leu Thr Glu Val Ala Thr Gly Gly	
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Ala Pro Leu Gly Lys Asp Val Ala Glu Ala Val Ala Lys Arg Leu Lys	
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Leu Pro Gly Ile Ile Gln Gly Tyr Gly Leu Thr Glu Thr Cys Cys Ala	
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Val Met Ile Thr Pro His Asn Ala Val Lys Thr Gly Ser Thr Gly Arg	
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ccc ttg cca tac att aaa gct aaa gtt tta gat aac gct act ggg aag	1156
Pro Leu Pro Tyr Ile Lys Ala Lys Val Leu Asp Asn Ala Thr Gly Lys	
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Asp Gly Asn Phe Phe Ile Val Asp Arg Leu Lys Glu Leu Ile Lys Tyr	
430 435 440	
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Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Asn Leu Leu Leu Gln	
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His Pro Ser Ile Ala Asp Ala Gly Val Thr Gly Val Pro Asp Glu Phe	
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Gly Gly Gln Leu Pro Ala Ala Cys Val Val Leu Glu Ser Gly Lys Thr	
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Leu Thr Glu Lys Glu Val Gln Asp Phe Ile Ala Ala Gln Val Thr Pro	
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Thr Lys His Leu Arg Gly Gly Val Val Phe Val Asp Ser Ile Pro Lys	
510 515 520	
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Gly Pro Thr Gly Lys Leu Ile Arg Lys Glu Leu Arg Glu Ile Phe Ala	
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 85 90 95
 Ile Pro Val Ala Thr Ser Asn Asp Met Tyr Thr Asp Gly Glu Leu Thr
 100 105 110
 Gly His Leu Asn Ile Ser Lys Pro Thr Ile Met Phe Ser Ser Lys Lys
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 Ala Leu Pro Leu Ile Leu Arg Val Gln Gln Asn Leu Ser Phe Ile Lys
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 Lys Val Val Val Ile Asp Ser Met Tyr Asp Ile Asn Gly Val Glu Cys
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 Val Ser Thr Phe Val Ala Arg Tyr Thr Asp His Thr Phe Asp Pro Leu
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 His Arg Ser Leu Thr Ile Arg Phe Val His Ser Arg Asp Pro Ile Tyr
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 Ala Glu Ala Val Ala Lys Arg Leu Lys Leu Pro Gly Ile Ile Gln Gly
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 Tyr Gly Leu Thr Glu Thr Cys Cys Ala Val Met Ile Thr Pro His Asn
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 Ala Val Lys Thr Gly Ser Thr Gly Arg Pro Leu Pro Tyr Ile Lys Ala
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 Lys Val Leu Asp Asn Ala Thr Gly Lys Ala Leu Gly Pro Gly Glu Arg
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 Gly Glu Ile Cys Phe Gln Ser Glu Met Ile Met Lys Gly Tyr Tyr Asn
 385 390 395 400
 Asn Pro Glu Ala Thr Ile Asp Thr Ile Asp Lys Asp Gly Trp Leu His
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Ser Gly Asp Ile Gly Tyr Tyr Asp Glu Asp Gly Asn Phe Phe Ile Val
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 Asp Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro
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 Gly Val Thr Gly Val Pro Asp Glu Phe Gly Gly Gln Leu Pro Ala Ala
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 Cys Val Val Leu Glu Ser Gly Lys Thr Leu Thr Glu Lys Glu Val Gln
 485 490 495
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 Gly Ile Ile Asp Ala His Thr Asn Glu Val Ile Ser Tyr Ala Gln Ile
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 Phe Glu Thr Ser Cys Arg Leu Ala Val Ser Leu Glu Lys Tyr Gly Leu
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 Asp His Asn Asn Val Val Ala Ile Cys Ser Glu Asn Asn Ile His Phe
 70 75 80 85
 ttt ggc cct tta att gct gct tta tac caa gga ata cca atg gca aca 343
 Phe Gly Pro Leu Ile Ala Ala Leu Tyr Gln Gly Ile Pro Met Ala Thr
 90 95 100

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Ser	Lys	Pro	Cys	Leu	Met	Phe	Cys	Ser	Lys	Lys	Ser	Leu	Pro	Phe	Ile	
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Leu	Lys	Val	Gln	Lys	His	Leu	Asp	Phe	Leu	Lys	Arg	Val	Ile	Val	Ile	
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Asp	Ser	Met	Tyr	Asp	Ile	Asn	Gly	Val	Glu	Cys	Val	Phe	Ser	Phe	Asp	
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Ile	Arg	Phe	Val	His	Ser	Ser	Asp	Pro	Ile	Tyr	Gly	Thr	Arg	Ile	Ala	
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cca	gat	aca	tca	att	ctt	gct	ata	gca	ccg	ttc	cat	cat	gcc	ttt	gga	775
Pro	Asp	Thr	Ser	Ile	Leu	Ala	Ile	Ala	Pro	Phe	His	His	Ala	Phe	Gly	
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Leu	Phe	Thr	Ala	Leu	Ala	Tyr	Phe	Pro	Val	Gly	Leu	Lys	Ile	Val	Met	
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gtg	aag	aaa	ttt	gag	ggc	gaa	ttc	ttc	tta	aaa	acc	ata	caa	aat	tac	871
Val	Lys	Lys	Phe	Glu	Gly	Glu	Phe	Phe	Leu	Lys	Thr	Ile	Gln	Asn	Tyr	
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Lys	Ile	Ala	Ser	Ile	Val	Val	Pro	Pro	Pro	Ile	Met	Val	Tyr	Leu	Ala	
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Lys	Ser	Pro	Leu	Val	Asp	Glu	Tyr	Asn	Cys	Ser	Ser	Leu	Thr	Glu	Ile	
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gct	agt	gga	ggc	tct	cct	tta	gga	aga	gat	atc	gca	gat	aaa	gta	gca	1015
Ala	Ser	Gly	Gly	Ser	Pro	Leu	Gly	Arg	Asp	Ile	Ala	Asp	Lys	Val	Ala	
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Gly Tyr Tyr Asp Glu Asp Arg Phe Ile Tyr Val Val Asp Arg Leu Lys	
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Glu Leu Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu	
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Asn Leu Leu Leu Gln His Pro Asn Ile Ser Asp Ala Gly Val Ile Glu	
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Phe Arg Thr Asn Leu Leu Val Asn Tyr Leu Ser Ala Cys Val Val Leu	
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Arg Ala Ile Phe Ala Arg Glu Gln Ala Lys Ser Lys Leu	
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Ala	Asp	Lys	Val	Ala	Lys	Arg	Leu	Lys	Val	His	Gly	Ile	Leu	Gln	Gly
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Val	Lys	Val	Ile	Asp	Ile	Asn	Thr	Gly	Lys	Ala	Leu	Gly	Pro	Arg	Glu
	370					375					380				
Lys	Gly	Glu	Ile	Cys	Phe	Lys	Ser	Gln	Met	Leu	Met	Lys	Gly	Tyr	His
385					390					395					400
Asn	Asn	Pro	Gln	Ala	Thr	Arg	Asp	Ala	Leu	Asp	Lys	Asp	Gly	Trp	Leu
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465					470					475					480	
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Lys	Leu															
545																

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 515
 520
 525
 530
 535
 540
 545

Headline

Filename : Phrixothrix vivianii lateral lanterns green light-eliciting
luciferase cDNA and deduced primary structure.
Sequence Size : 1746
Sequence Position: -25 - 1746

Translation Position: 1 - 1635;

Genetic Code : Universal (amino-acid residues are in 3 letter code)

-20 -10
TCAGTGCAAGACTTTAGGG

10	20	30	40	50	
ATCAAAATGGAAGAAGAAACATTAGGCATGGAGAGCGTCCTCGTGATATAGTCCATCCT					
MetGluGluGluAsnIleArgHisGlyGluArgProArgAspIleValHisPro					
60	70	80	90	100	110
GGCTCGGCAGGACAACAATTATACCAATCATTGTATAAATTTGCATCCTTTTCCTGAAGCA					
GlySerAlaGlyGlnGlnLeuTyrGlnSerLeuTyrLysPheAlaSerPheProGluAla					
120	130	140	150	160	170
ATAATCGATGCTCATACAAATGAAGTAATATCATATGCTCAAATATTTGAAACCAGCTGC					
IleIleAspAlaHisThrAsnGluValIleSerTyrAlaGlnIlePheGluThrSerCys					
180	190	200	210	220	230
CGCTTAGCTGTTAGTATAGAACAATATGGCTTGAATGAAAACAATGTTGTGGGTGTATGC					
ArgLeuAlaValSerIleGluGlnTyrGlyLeuAsnGluAsnAsnValValGlyValCys					
240	250	260	270	280	290
AGTGAAPACAATATTAACCTTTTTTAATCCTGCTCCTTGCTGCTTTTACTTAGGAATACCA					
SerGluAsnAsnIleAsnPhePheAsnProValLeuAlaAlaLeuTyrLeuGlyIlePro					
300	310	320	330	340	350
GTAGCAACATCAAATGATATGTACACAGATGGAGAGTTAACTGGTCATTTGAATATATCA					
ValAlaThrSerAsnAspMetTyrThrAspGlyGluLeuThrGlyHisLeuAsnIleSer					
360	370	380	390	400	410
AAACCAACTATCATGTTTAGTTCAAAGAAAGCACTCCCGCTTATTCTGAGAGTACAGCAA					
LysProThrIleMetPheSerSerLysLysAlaLeuProLeuIleLeuArgValGlnGln					
420	430	440	450	460	470
AATCTAAGTTTTCATTAAAAAAGTCGTAGTTATCGATAGCATGTACGACATTAATGGCGTT					
AsnLeuSerPheIleLysLysValValValIleAspSerMetTyrAspIleAsnGlyVal					
480	490	500	510	520	530
GAATGCGTATCTACCTTTGTTGCAAGTTTATACTGACCACACCTTTGATCCATTGTCATTT					
GluCysValSerThrPheValAlaArgTyrThrAspHisThrPheAspProLeuSerPhe					
540	550	560	570	580	590
ACACCAAAAGATTTTGATCCCCTTGAAAAAATCGCATTAAATTATGTCATCATCTGGAACA					
ThrProLysAspPheAspProLeuGluLysIleAlaLeuIleMetSerSerSerGlyThr					

FIG. 1A

600 610 620 630 640 650
 ACTGGATTGCCTAAGGGTGTAGTACTGAGCCATAGAAGTCTAACTATAAGATTCGTTTCAT
 ThrGlyLeuProLysGlyValValLeuSerHisArgSerLeuThrIleArgPheValHis
 660 670 680 690 700 710
 AGCAGGGATCCCATTATGGCACTCGTACGGTTCCACAAACATCAATTCTTTCCCTTAGTA
 SerArgAspProIleTyrGlyThrArgThrValProGlnThrSerIleLeuSerLeuVal
 720 730 740 750 760 770
 CCGTTCCATCATGCCTTTGGAAATGTTTACTACATTATCTTACTTTGTAGTAGGACTTAAG
 ProPheHisHisAlaPheGlyMetPheThrThrLeuSerTyrPheValValGlyLeuLys
 780 790 800 810 820 830
 GTTGTAATGTTGAAGAAATTTGAGGGCGCACTTTTCTTAAAACCATACAGAATTACAAA
 ValValMetLeuLysLysPheGluGlyAlaLeuPheLeuLysThrIleGlnAsnTyrLys
 840 850 860 870 880 890
 ATCCCCACTATTGTAGTGGCCCCCTCCAGTTATGGTGTGTTTTGGCTAAAAGCCCCATTAGTC
 IleProThrIleValValAlaProProValMetValPheLeuAlaLysSerProLeuVal
 900 910 920 930 940 950
 GATCAATACGATTTATCGAGCTTAACGGAAGTTGCTACTGGAGGAGCTCCTTTAGGAAAA
 AspGlnTyrAspLeuSerSerLeuThrGluValAlaThrGlyGlyAlaProLeuGlyLys
 960 970 980 990 1000 1010
 GATGTCGCAGAAGCAGTAGCAGAGAGGTTGAAATTACCTGGAATCATAAAGGATATGGA
 AspValAlaGluAlaValAlaLysArgLeuLysLeuProGlyIleIleGlnGlyTyrGly
 1020 1030 1040 1050 1060 1070
 TTAAGTGAAGCTTGCTGCGCTGTAATGATTACCCCTCATATGCTGTGAAGCAGGTTCA
 LeuThrGluThrCysCysAlaValMetIleThrProHisAsnAlaValLysThrGlySer
 1080 1090 1100 1110 1120 1130
 ACTGGAAGACCCTTGCCATACATTAAAGCTAAAGTTTTAGATAACGCTACTGGGAAGGCG
 ThrGlyArgProLeuProTyrIleLysAlaLysValLeuAspAsnAlaThrGlyLysAla
 1140 1150 1160 1170 1180 1190
 CTAGGACCAGGAGAAAGAGGCGAAATATGCTTTCAAAGTGAAATGATTATGAAAGGATAT
 LeuGlyProGlyGluArgGlyGluIleCysPheGlnSerGluMetIleMetLysGlyTyr
 1200 1210 1220 1230 1240 1250
 TACAACAATCCGGAAGCAACTATTGATACTATTGACAAAGATGGTTGGCTTCATTCTGGA
 TyrAsnAsnProGluAlaThrIleAspThrIleAspLysAspGlyTrpLeuHisSerGly
 1260 1270 1280 1290 1300 1310
 GATATTGGATATTACGACGAAGATGGAAATTTCTTTATAGTTGATCGATTGAAAGAACTT
 AspIleGlyTyrTyrAspGluAspGlyAsnPhePheIleValAspArgLeuLysGluLeu
 1320 1330 1340 1350 1360 1370
 ATTAAATACAAGGGATATCAGGTTGCGCCTGCTGAACTGGAAAATCTGCTTTTACAACAT
 IleLysTyrLysGlyTyrGlnValAlaProAlaGluLeuGluAsnLeuLeuLeuGlnHis
 1380 1390 1400 1410 1420 1430
 CCAAGTATTGCTGATGCGGGTGTACTGGAGTTCCGGACGAATTTGGTGGACAATTACCT
 ProSerIleAlaAspAlaGlyValThrGlyValProAspGluPheGlyGlyGlnLeuPro

Insert
A

FIG. 1B

1440 1450 1460 1470 1480 1490
GCTGCTTGTGTTGTGTTAGAATCTGGCAAGACGCTGACTGAAAAGGAAGTTCAAGATTTT
AlaAlaCysValValLeuGluSerGlyLysThrLeuThrGluLysGluValGlnAspPhe

1500 1510 1520 1530 1540 1550
ATTGCAGCACAAGTCACTCCAACAAAGCATCTTCGAGGCGGTGTCGTATTTGTAGACAGT
IleAlaAlaGlnValThrProThrLysHisLeuArgGlyGlyValValPheValAspSer

1560 1570 1580 1590 1600 1610
ATTCCGAAAGGCCCTACTGGAAAACATCAGAAAGGAGCTCCGAGAAATATTTGCCCCAG
IleProLysGlyProThrGlyLysLeuIleArgLysGluLeuArgGluIlePheAlaGln

1620 1630 1640
CGAGCACCAAAATCAAAATTATAAGTTCAATGTATTGCTTTAGTTCTAAAATGTATATAA
ArgAlaProLysSerLysLeu***

ACAAGTTTTAGAACCTAATACATTCATTCAAATACTAAACAAAAAAAAAAAAAAAAAAAAA
1740
AAAAAA

FIG. 1C